



SEQUENCE LISTING

<110> Dunn-Coleman, Nigel
Langdon, Timothy
Morse, Phillip

<120> Manipulation of the Phenolic Acid
Content and Digestibility of Plant Cell Walls by Targeted
Expression of Genes Encoding Cell Wall Degrading Enzymes

<130> GC648-2

<140> US 09/991,209

<141> 2001-11-16

<150> US 60/249,608

<151> 2000-11-17

<160> 97

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> *Aspergillus niger*

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 <213> *Aspergillus niger*

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35     40     45
Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn
50     55     60
Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp Asp Ser Ser Lys
65     70     75     80
Glu Ile Ile Thr Val Phe Arg Gly Thr Gly Ser Asp Thr Asn Leu Gln
85     90     95
Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr Leu Pro Gln Cys
100    105    110
Asn Gly Cys Glu Val His Gly Gly Tyr Tyr Ile Gly Trp Val Ser Val
115    120    125
Gln Asp Gln Val Glu Ser Leu Val Lys Gln Gln Val Ser Gln Tyr Pro
130    135    140
Asp Tyr Ala Leu Thr Val Thr Gly His Ser Leu Gly Ala Ser Leu Ala
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Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp Asn Ile Arg Leu
165    170    175
Tyr Thr Phe Gly Glu Pro Arg Ser Gly Asn Gln Ala Phe Ala Ser Tyr
180    185    190
Met Asn Asp Ala Phe Gln Ala Ser Ser Pro Asp Thr Thr Gln Tyr Phe
195    200    205
Arg Val Thr His Ala Asn Asp Gly Ile Pro Asn Leu Pro Pro Val Glu
210    215    220
Gln Gly Tyr Ala His Gly Gly Val Glu Tyr Trp Ser Val Asp Pro Tyr
225    230    235    240
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Glu Ala Gln Gly Gly Gln Gly Val Asn Asn Ala His Thr Thr Tyr Phe
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<212> DNA

<213> Artificial Sequence

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<223> inactivated PCR product reading frame

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35

<210> 5

<211> 10

<212> PRT

<213> Artificial Sequence

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<223> retention sequence

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<210> 6

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> retention sequence encoding sequence

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<211> 15

<212> PRT

<213> Artificial Sequence

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<223> FAE-linker-frameshift sequence

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<210> 8

<211> 48

<212> DNA

<213> Artificial Sequence

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<223> FAE-linker-frameshift sequence

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<210> 9

<211> 41

<212> PRT

<213> Hordeum sp.

<400> 9

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		20					25						30		
Ile	Arg	Pro	Val	Thr	Asp	Arg	Ala	Ala							
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<211> 134

<212> DNA

<213> Hordeum sp.

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<211> 46

<212> PRT

<213> Rattus sp.

<400> 11

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		20						25					30		
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<211> 149

<212> DNA

<213> Rattus sp.

<400> 12

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<212> PRT

<213> Solanum sp.

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<221> VARIANT

<222> (1)...(50)

<223> Xaa = Any Amino Acid

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 <212> DNA
 <213> Solanum sp.

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 <212> DNA
 <213> Artificial Sequence

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 <223> pTP10-1 vector

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 <223> Xaa = Any Amino Acid

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 <213> Artificial Sequence

<220>
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 Lys Ile Tyr Asn Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp
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 Asp Ser Ser Lys Glu Ile Ile Thr Val Phe Arg Gly Thr Gly Ser Asp
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 Thr Asn Leu Gln Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr
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 Leu Pro Gln Cys Asn Gly Cys Glu Val His Gly Gly Tyr Tyr Ile Gly
 130 135 140
 Trp Val Ser Val Gln Asp Gln Val Glu Ser Leu Val Lys Gln Gln Val
 145 150 155 160
 Ser Gln Tyr Pro Asp Tyr Ala Leu Thr Val Thr Gly His Xaa Leu Gly
 165 170 175
 Ala Ser Leu Ala Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp
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 <211> 5395
 <212> DNA
 <213> Artificial Sequence

<220>

<223> pTT5.14 vector

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<210> 22
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<212> PRT
<213> Artificial Sequence

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<220>
<223> pTT5.14 vector

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<223> Xaa = Any Amino Acid

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 35             40             45
Glu Asp Leu Tyr Ser Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala
 50             55             60
Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu
 65             70             75             80
Lys Ile Tyr Asn Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp
 85             90             95

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<212> DNA

<213> Artificial Sequence

<220>

<223> pTP8-5 vector

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<210> 24
<211> 306
<212> PRT
<213> Artificial Sequence

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<220>
<223> pTP8-5 vector

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<221> VARIANT
<222> (1)...(306)
<223> Xaa = Any Amino Acid

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35          40          45
Glu Asp Leu Tyr Ser Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala
50          55          60
Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu
65          70          75          80
Lys Ile Tyr Asn Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp
85          90          95
Asp Ser Ser Lys Glu Ile Ile Thr Val Phe Arg Gly Thr Gly Ser Asp
100         105         110
Thr Asn Leu Gln Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr
115         120         125
Leu Pro Gln Cys Asn Gly Cys Glu Val His Gly Gly Tyr Tyr Ile Gly
130         135         140
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145         150         155         160
Ser Gln Tyr Pro Asp Tyr Ala Leu Thr Val Thr Gly His Xaa Leu Gly
165         170         175
Ala Ser Leu Ala Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp
180         185         190
Asn Ile Arg Leu Tyr Thr Phe Gly Glu Pro Arg Ser Gly Asn Gln Ala
195         200         205
Phe Ala Ser Tyr Met Asn Asp Ala Phe Gln Ala Ser Ser Pro Asp Thr
210         215         220
Thr Gln Tyr Phe Arg Val Thr His Ala Asn Asp Gly Ile Pro Asn Leu
225         230         235         240
Pro Pro Val Glu Gln Gly Tyr Ala His Gly Gly Val Glu Tyr Trp Ser
245         250         255
Val Asp Pro Tyr Ser Ala Gln Asn Thr Phe Val Cys Thr Gly Asp Glu
260         265         270
Val Gln Cys Cys Glu Ala Gln Gly Gly Gln Gly Val Asn Asn Ala His
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305

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<210> 25
 <211> 5277
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pTP5-1 vector

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<212> PRT

<213> Artificial Sequence

<220>

<223> pTP5-1 vector

<221> VARIANT

<222> (1)...(293)

<223> Xaa = Any Amino Acid

<400> 26

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Ser Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala Ala Tyr Ala Asp
      35             40             45
Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn
      50             55             60
Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp Asp Ser Ser Lys

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<210> 27

<211> 5327

<212> DNA

<213> Artificial Sequence

<220>

<223> pTP4a2 vector

<400> 27

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[illegible]

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 50           55           60
Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu
 65           70           75           80
Lys Ile Tyr Asn Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp
 85           90           95
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Thr Asn Leu Gln Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr
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<211> 299

<212> PRT

<213> Artificial Sequence

<220>

<223> pUG4 vector

<221> VARIANT

<222> (1)...(299)

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<210> 42

<211> 301

<212> PRT

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<220>

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<222> (1)...(301)

<223> Xaa = Any Amino Acid

<400> 42

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Ile Arg Pro Val Thr Asp Arg Ala Ala Ala Ser Thr Gln Gly Ile Ser
35          40          45
Glu Asp Leu Tyr Ser Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala
50          55          60
Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu
65          70          75          80
Lys Ile Tyr Asn Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp
85          90          95
Asp Ser Ser Lys Glu Ile Ile Thr Val Phe Arg Gly Thr Gly Ser Asp
100         105         110
Thr Asn Leu Gln Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr
115         120         125
Leu Pro Gln Cys Asn Gly Cys Glu Val His Gly Gly Tyr Tyr Ile Gly
130         135         140
Trp Val Ser Val Gln Asp Gln Val Glu Ser Leu Val Lys Gln Gln Val
145         150         155         160
Ser Gln Tyr Pro Asp Tyr Ala Leu Thr Val Thr Gly His Xaa Leu Gly
165         170         175
Ala Ser Leu Ala Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp
180         185         190
Asn Ile Arg Leu Tyr Thr Phe Gly Glu Pro Arg Ser Gly Asn Gln Ala
195         200         205
Phe Ala Ser Tyr Met Asn Asp Ala Phe Gln Ala Ser Ser Pro Asp Thr
210         215         220
Thr Gln Tyr Phe Arg Val Thr His Ala Asn Asp Gly Ile Pro Asn Leu
225         230         235         240
Pro Pro Val Glu Gln Gly Tyr Ala His Gly Gly Val Glu Tyr Trp Ser
245         250         255
Val Asp Pro Tyr Ser Ala Gln Asn Thr Phe Val Cys Thr Gly Asp Glu
260         265         270
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 290 295 300

<210> 43
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 agtaaaatat cggtaataaa aggtggccca aagtgaattt tactcttttc tactattata 180
 aaaattgagg atgttttggt ggtactttga tacgtcattt ttgtatgaat tggtttttaa 240
 gttttattcg gatttgaaa tgcataatctg tatttgagtc ggtttttaag ttcgttgctt 300
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 cataattttt gagaaaaata tatattcagg cgaattccac aatgaacaat aataagatta 420
 aaatagcttg cccccgttg agcgatgggt attttttcta gtaaaataaa agataaactt 480
 agactcaaaa catttacaaa aacaacccct aaagtcctaa agcccaaagt gctatgcacg 540
 atccatagca agcccagccc aacccaaccc aacccaaccc accccagtgc agccaactgg 600
 caaatagtct ccacccccgg cactatcacc gtgagttgtc cgcaccaccg cacgtctcgc 660
 agccaaaaaa aaaaaaagaa agaaaaaaa gaaaaagaaa aacagcaggt ggggtccgggt 720
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 cgtgagtcgg ccggtatcct cgcggggaat ggggctctcg gatgtagatc ttctttcttt 1140
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<210> 44
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> aleurain-NPIR delete structure

<400> 44
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 1 5 10 15
 Ala Ala Val Ala Val Ala Ser Ser Arg Ala Ala
 20 25

<210> 45
 <211> 93
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> aleurain-NPIR delete structure encoding sequence

<400> 45
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 gccgtcgccg tcgctcctc ccgcgcggcc gcc 93

<210> 46
 <211> 873
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> SEE1 (senescence enhanced) promoter

<400> 46
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 ctagatagca cagccacagc acctacagga gtgcgacact tgtggactgt agtagtggtg 180
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 tctcaaccaa tcacgcgctc ccaacaaaat atcgcccccc atgtcttggt ggagagagag 300
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 gctcccggga gctcactcat tcaagatccc atcgctcgtc tcacccctgg cgtcatggga 420
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 ataaccat tccagattccc ccaatagaga aagtatagca tgctttcggg ttttgtttg 540
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 gcagagcctg aagcaagtgg tgaagcgtgg cgatgagatg ggtataaaac ccccgacc 780
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<210> 47
 <211> 39
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEE1 promoter plus vacuolar aleurain signal/NPIR
 sequence

<400> 47
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 20 25 30
 Val Thr Glu Arg Ala Ala Ala
 35

<210> 48
 <211> 987
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> SEE1 promoter plus vacuolar aleurain signal/NPIR
 encoding sequence

<221> misc_feature
 <222> (1)...(987)
 <223> n = A,T,C or G

<400> 48
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gctcccggga	gctcactcat	tcaagatccc	atcgctcgctg	tcacccctgg	cgatcatggga	420
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ctcgcgctct	tggccaccgc	cgcggtggcc	gccgcatact	tggcgggactc	caacccgatc	960
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<210> 49

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 49

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<210> 50

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 50

ccggccacgc	cctcggcgcc	tccctggcgg	cactc	35
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<210> 51

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 51

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<210> 52

<211> 50

<212> DNA

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<220>

<223> primer

<400> 52

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<211> 325
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<220>

<223> amplified nos terminator sequence from pMA406
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<400> 53

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tatcatataa tttctgttga attacgttaa gcatgtaata attaacaatgt aatgcatgac	180
gttattttatg agatggggtt ttatgattag agtcccgcga ttatacattt aatacgcgat	240
agaaaacaaa atatagcgcg caaactagga taaattatcg cgcgcggtgt catctatgtt	300
actagatcga taagcttcta gatct	325

<210> 54

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 54

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ttcaaacatt tg	72

<210> 55

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 55

aagactgcag accatggcgg	20
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<210> 56

<211> 40

<212> DNA

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<220>

<223> primer

<400> 56

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<210> 57

<211> 33

<212> DNA

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<220>

<223> primer

<400> 57

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<210> 58
 <211> 36
 <212> DNA
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<220>
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<400> 58
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<210> 59
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<220>
 <223> primer

<400> 59
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<210> 60
 <211> 10
 <212> DNA
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<220>
 <223> Accl site

<400> 60
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<210> 61
 <211> 39
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<220>
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<400> 61
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<210> 62
 <211> 36
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<220>
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<400> 62
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<210> 63
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<220>
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 <400> 63
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 <210> 64
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 <220>
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 <400> 64
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 <210> 65
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 <220>
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 <400> 65
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 <210> 66
 <211> 55
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 <220>
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 <400> 66
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 <210> 67
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 <220>
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 <400> 67
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 <210> 68
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 <220>
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 <400> 68

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<210> 69
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<220>
 <223> primer

<400> 69
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<210> 70
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<220>
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<400> 70
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<210> 71
 <211> 45
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<220>
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<400> 71
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<220>
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<210> 73
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<220>
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<210> 74
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<400> 77
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<220>
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<400> 78
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<210> 79
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<400> 79

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<210> 80

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<210> 81

<211> 39

<212> DNA

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<223> primer

<400> 81

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<210> 82

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 82

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<210> 83

<211> 32

<212> DNA

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<220>

<223> primer

<400> 83

ctaaagctta acatgaagca gttctccgcc aa

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<210> 84

<211> 8

<212> DNA

<213> Oryza sp.

<400> 84

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<210> 85

<211> 7

<212> PRT

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<223> KDEL fusion peptide

<400> 85

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<210> 86

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> designated KDEL fusion peptide

<400> 86

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1 5

<210> 87

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> frameshifted terminal peptide

<400> 87

Glu Thr Thr Glu Gly
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<210> 88

<211> 27

<212> PRT

<213> Aspergillus niger

<400> 88

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20 25

<210> 89

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<213> Aspergillus niger

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<210> 90

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<223> ER retention vector

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<220>
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<400> 91
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<210> 92
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<220>
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<400> 92
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<210> 93
 <211> 8
 <212> PRT
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<220>
 <223> ferulic esterase end

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 Cys Thr Trp Pro Val Ala Ala Ala
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<210> 94
 <211> 72
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pTP4a2 vector

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 20 25 30
 Ser Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala Ala Tyr Ala Asp
 35 40 45
 Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn
 50 55 60
 Ser Gln Thr Asp Ile Asn Gly Trp
 65 70

<210> 95
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> protein encoded by functional reading frame

<400> 95
 Tyr Ala Leu Thr Val Thr Gly His Ser Leu Gly Ala Ser Leu Ala Ala
 1 5 10 15
 Leu

<210> 96
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> protein encoded by inactivated reading frame

<400> 96
 Tyr Ala Leu Thr Val Thr Gly His Ala Leu Gly Ala Ser Leu Ala Ala
 1 5 10 15
 Leu

<210> 97
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> retention sequence

<400> 97
 Lys Asp Glu Leu
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